RAW SEQUENCE LISTING
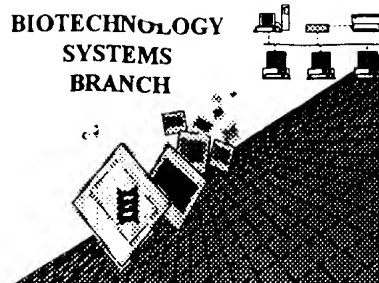# ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/848,353_

Source: _OIPE_

Date Processed by STIC: _6/5/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/09/848,353**

DATE: 06/05/2001
TIME: 13:37:26

Input Set : **A:\seq.lst.final.txt**
Output Set: **C:\CRF3\06052001\I848353.raw**

Does Not Comply
Correct Diskette Needed

py 1-2

```
  6 <110> APPLICANT: Staddon, James M.
  7          Rubin, Lee L.
  8          Herrenknecht, Kurt
  9          Morgan, Mary L.
 14 <120> TITLE OF INVENTION: Modulating the Permeability of a Physiological Barrier With
an Agent
 15          That Modulates Tyrosine Phosphorylation
 19 <130> FILE REFERENCE: 0623.0410001
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→ **24 <140> CURRENT APPLICATION NUMBER: US/09/848,353**
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 27 <141> CURRENT FILING DATE: 2001-05-04
 32 <150> PRIOR APPLICATION NUMBER: US 08/648,182
 35 <151> PRIOR FILING DATE: 1997-12-23
 40 <150> PRIOR APPLICATION NUMBER: PCT/GB94/02543
 43 <151> PRIOR FILING DATE: 1994-11-18
 48 <150> PRIOR APPLICATION NUMBER: GB 9323884.8
 51 <151> PRIOR FILING DATE: 1993-11-19
 59 <160> NUMBER OF SEQ ID NOS: 9
 65 <170> SOFTWARE: PatentIn Ver. 2.0
 71 <210> SEQ ID NO: 1
 74 <211> LENGTH: 11
 77 <212> TYPE: PRT
 80 <213> ORGANISM: Organism: Homo sapiens
 84 <400> SEQUENCE: 1
 87 Asn Ile Ser Phe Gly Arg Asp Gln Asp Asn Lys
 92 <210> SEQ ID NO: 2
 95 <211> LENGTH: 7
 98 <212> TYPE: PRT
101 <213> ORGANISM: Organism: Homo sapiens
105 <400> SEQUENCE: 2
108 His Ala Ile Pro Asn Leu Val
109      1              5
114 <210> SEQ ID NO: 3
117 <211> LENGTH: 6
120 <212> TYPE: PRT
123 <213> ORGANISM: Organism: Homo sapiens
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W--> **126 <220> FEATURE: Feature:**
W--> **128 <221> NAME/KEY: Name/Key: Modified site**
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130 <222> LOCATION: Location: 1
132 <223> OTHER INFORMATION: Other Information: /note= "Xaa at residue 1 = any
133          amino acid"
137 <400> SEQUENCE: 3
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W--> **140 Xaa Val Leu Ile Asn Lys**
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141      1              5
146 <210> SEQ ID NO: 4
149 <211> LENGTH: 15
152 <212> TYPE: PRT
155 <213> ORGANISM: Organism: Homo sapiens
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W--> **158 <220> FEATURE: Feature:**

delete - do not use alphabetical headings when using new sequence ruler format

(FYI: The CRF program automatically inserts alphabetical headings for clarity.)

RAW SEQUENCE LISTING   DATE: 06/05/2001
PATENT APPLICATION: US/09/848,353   TIME: 13:37:26

Input Set : A:\seq.lst.final.txt
Output Set : C:\CRF3\06052001\I848353.raw

W--> 160 <221> NAME/KEY: Name/Key: Modified site
     162 <222> LOCATION: Location: 1..15
     164 <223> OTHER INFORMATION: Other Information: /note= "Xaa at residues 1 and 15 = any
     165   amino acid"
     169 <400> SEQUENCE: 4
W--> 173 Xaa Pro Ile Glu Asp Pro Ala Asn Asp Thr Val Asp Phe Pro Xaa
     174   1   5   10   15
     179 <210> SEQ ID NO: 5
     182 <211> LENGTH: 15
     185 <212> TYPE: PRT
     188 <213> ORGANISM: Organism: Homo sapiens
W--> 191 <220> FEATURE: Feature:
W--> 193 <221> NAME/KEY: Name/Key: Modified site
     195 <222> LOCATION: Location: 1..15
     197 <223> OTHER INFORMATION: Other Information: /note= "Xaa at residues 1 and 15 = any
     198   amino acid"
     202 <400> SEQUENCE: 5
W--> 206 Xaa Pro Ser Gly Ala Leu Arg Asn Leu Ala Val Asp Ala Arg Xaa
     207   1   5   10   15
     212 <210> SEQ ID NO: 6
     215 <211> LENGTH: 7
     218 <212> TYPE: PRT
     221 <213> ORGANISM: Organism: Mus musculus
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     228 His Ala Arg Pro Asn Leu Val
     229   1   5
     235 <210> SEQ ID NO: 7
     238 <211> LENGTH: 6
     241 <212> TYPE: PRT
     244 <213> ORGANISM: Organism: Mus musculus
     249 <400> SEQUENCE: 7
     251 Leu Val Leu Ile Asn Lys
     252   1   5
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     263 <212> TYPE: PRT
     266 <213> ORGANISM: Organism: Mus musculus
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     273 <222> LOCATION: Location: 15
     275 <223> OTHER INFORMATION: Other Information: /note= "Xaa at residue 15 = any
     276   amino acid"
     280 <400> SEQUENCE: 8
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     283   1   5   10   15
     288 <210> SEQ ID NO: 9
     291 <211> LENGTH: 15
     294 <212> TYPE: PRT
     297 <213> ORGANISM: Organism: Mus musculus

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/848,353

DATE: 06/05/2001
TIME: 13:37:26

Input Set : A:\seq.lst.final.txt
Output Set: C:\CRF3\06052001\I848353.raw

302 <400> SEQUENCE: 9
305 Ala Ala Ser Gly Ala Leu Arg Asn Leu Ala Val Asp Ala Arg Lys
306   1   5   10   15

VERIFICATION SUMMARY   DATE: 06/05/2001
PATENT APPLICATION: **US/09/848,353**   TIME: 13:37:27

Input Set : **A:\seq.lst.final.txt**
Output Set: **C:\CRF3\06052001\I848353.raw**

L:24 M:270 C: Current Application Number differs, Replaced Current Application Number
L:126 M:256 W: Invalid Numeric Header Field, ·220· has non-blank data
L:128 M:257 W: Feature value mis-spelled or invalid, ·221· Name/Key for SEQ ID#:3
L:140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:158 M:256 W: Invalid Numeric Header Field, ·220· has non-blank data
L:160 M:257 W: Feature value mis-spelled or invalid, ·221· Name/Key for SEQ ID#:4
L:173 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:191 M:256 W: Invalid Numeric Header Field, ·220· has non-blank data
L:193 M:257 W: Feature value mis-spelled or invalid, ·221· Name/Key for SEQ ID#:5
L:206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:269 M:256 W: Invalid Numeric Header Field, ·220· has non-blank data
L:271 M:257 W: Feature value mis-spelled or invalid, ·221· Name/Key for SEQ ID#:8
L:282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8